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16

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<400> 4  
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17

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<223> invertase leader sequence

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<223> first 5 amino acids of mature human serum albumin

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Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys  
1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser  
20

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<211> 21

<212> DNA

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21

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

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gatcctgtgg cttcgatgca cacaaga

27

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24

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62

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fragments with non-cohesive ends.
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Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu	
1				5					10					15		
gaa	aat	ttc	aaa	gcc	ttg	gtg	ttg	att	gcc	ttt	gct	cag	tat	ctt	cag	96
Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln	
			20					25					30			
cag	tgt	cca	ttt	gaa	gat	cat	gta	aaa	tta	gtg	aat	gaa	gta	act	gaa	144
Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu	
		35					40					45				
ttt	gca	aaa	aca	tgt	gtt	gct	gat	gag	tca	gct	gaa	aat	tgt	gac	aaa	192
Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys	
50						55					60					
tca	ctt	cat	acc	ctt	ttt	gga	gac	aaa	tta	tgc	aca	gtt	gca	act	ctt	240
Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu	
65					70					75					80	
cgt	gaa	acc	tat	ggg	gaa	atg	gct	gac	tgc	tgt	gca	aaa	caa	gaa	cct	288
Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro	
				85					90					95		
gag	aga	aat	gaa	tgc	ttc	ttg	caa	cac	aaa	gat	gac	aac	cca	aac	ctc	336
Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	Leu	
			100					105					110			
ccc	cga	ttg	gtg	aga	cca	gag	gtt	gat	gtg	atg	tgc	act	gct	ttt	cat	384
Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	His	
		115					120					125				

[illegible]

[illegible]



099718-0411

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
1 5 10 15

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
290 295 300



Leu 305	Ala	Ala	Asp	Phe	Val 310	Glu	Ser	Lys	Asp	Val 315	Cys	Lys	Asn	Tyr	Ala 320
Glu	Ala	Lys	Asp	Val 325	Phe	Leu	Gly	Met	Phe 330	Leu	Tyr	Glu	Tyr	Ala 335	Arg
Arg	His	Pro	Asp 340	Tyr	Ser	Val	Val	Leu 345	Leu	Leu	Arg	Leu	Ala 350	Lys	Thr
Tyr	Glu	Thr 355	Thr	Leu	Glu	Lys	Cys 360	Cys	Ala	Ala	Ala	Asp 365	Pro	His	Glu
Cys	Tyr 370	Ala	Lys	Val	Phe	Asp 375	Glu	Phe	Lys	Pro	Leu 380	Val	Glu	Glu	Pro
Gln 385	Asn	Leu	Ile	Lys	Gln 390	Asn	Cys	Glu	Leu	Phe 395	Glu	Gln	Leu	Gly	Glu 400
Tyr	Lys	Phe	Gln 405	Asn	Ala	Leu	Leu	Val	Arg 410	Tyr	Thr	Lys	Lys	Val 415	Pro
Gln	Val	Ser	Thr 420	Pro	Thr	Leu	Val	Glu 425	Val	Ser	Arg	Asn	Leu	Gly	Lys
Val	Gly 435	Ser	Lys	Cys	Cys	Lys	His 440	Pro	Glu	Ala	Lys	Arg 445	Met	Pro	Cys
Ala	Glu 450	Asp	Tyr	Leu	Ser	Val 455	Val	Leu	Asn	Gln	Leu 460	Cys	Val	Leu	His
Glu 465	Lys	Thr	Pro	Val	Ser	Asp 470	Arg	Val	Thr	Lys 475	Cys	Cys	Thr	Glu	Ser 480
Leu	Val	Asn	Arg 485	Arg	Pro	Cys	Phe	Ser	Ala 490	Leu	Glu	Val	Asp	Glu 495	Thr
Tyr	Val	Pro	Lys 500	Glu	Phe	Asn	Ala	Glu 505	Thr	Phe	Thr	Phe	His 510	Ala	Asp
Ile	Cys	Thr 515	Leu	Ser	Glu	Lys	Glu 520	Arg	Gln	Ile	Lys	Lys 525	Gln	Thr	Ala
Leu 530	Val	Glu	Leu	Val	Lys	His 535	Lys	Pro	Lys	Ala	Thr 540	Lys	Glu	Gln	Leu
Lys 545	Ala	Val	Met	Asp	Asp 550	Phe	Ala	Ala	Phe	Val 555	Glu	Lys	Cys	Cys	Lys 560
Ala	Asp	Asp	Lys	Glu 565	Thr	Cys	Phe	Ala	Glu 570	Glu	Gly	Lys	Lys	Leu 575	Val
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<210> 21

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<211> 60

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<221> Misc\_Structure

<223> Synthetic oligonucleotide used to alter restriction sites in pPPC0007

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<211> 60

<212> DNA

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<221> Misc\_Structure

<223> Synthetic oligonucleotide used to alter restriction sites in pPPC0007

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<210> 25

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<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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0983318-041201

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32

<210> 26

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<212> DNA

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<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein



09033110-041201

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0903110-041201

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1 5 10 15  
Tyr Ser Arg Ser Leu Asp Lys Arg  
20

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040313.041201

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46

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09033118-041201

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<213> Artificial Sequence

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<221> signal

<223> Stanniocalcin signal peptide

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Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser  
1 5 10 15

Ala

<210> 35

<211> 22

<212> PRT

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<220>

<221> signal

<223> Synthetic signal peptide

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Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Ala Leu  
1 5 10 15

Trp Ala Pro Ala Arg Gly  
20